

SEQUENCE LISTING

<110> Salonen, Jukka T

<120> Method for detecting a risk of hypertension and uses thereof

<130> Alpha-2B-AR variant

<140>

<141>

<160> 10

<170> PatentIn Ver. 2.1

<210> 1

<211> 1344

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1) . . (1341)

<223> Coding sequence for variant human alpha-2B-adrenoceptor protein

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gcg gcc atc acc ttc ctc att ctc ttt acc atc ttc ggc aac gct ctg 96
Ala Ala Ile Thr Phe Leu Ile Leu Phe Thr Ile Phe Gly Asn Ala Leu
20 25 30

gtc atc ctg gct gtg ttg acc agc cgc tgc ctg cgc gcc cct cag aac 144
Val Ile Leu Ala Val Leu Thr Ser Arg Ser Leu Arg Ala Pro Gln Asn
35 40 45

ctg ttc ctg gtg tcg ctg gcc gcc gcc gac atc ctg gtg gcc acg ctc 192
Leu Phe Leu Val Ser Leu Ala Ala Ala Asp Ile Leu Val Ala Thr Leu
50 55 60

atc atc cct ttc tgc ctg gcc aac gag ctg ctg ggc tac tgg tac ttc 240
Ile Ile Pro Phe Ser Leu Ala Asn Glu Leu Leu Gly Tyr Trp Tyr Phe
65 70 75 80

cgg cgc acg tgg tgc gag gtg tac ctg gcg ctc gac gtg ctc ttc tgc 288
Arg Arg Thr Trp Cys Glu Val Tyr Leu Ala Leu Asp Val Leu Phe Cys
 85 90 95

acc tcg tcc atc gtg cac ctg tgc gcc atc agc ctg gac cgc tac tgg 336
Thr Ser Ser Ile Val His Leu Cys Ala Ile Ser Leu Asp Arg Tyr Trp
100 105 110

gcc gtg agc cgc gcg ctg gag tac aac tcc aag cgc acc ccg cgc cgc 384
Ala Val Ser Arg Ala Leu Glu Tyr Asn Ser Lys Arg Thr Pro Arg Arg
115 120 125

atc aag tgc atc atc ctc act gtg tgg ctc atc gcc gcc gtc atc tcg 432
Ile Lys Cys Ile Ile Leu Thr Val Trp Leu Ile Ala Ala Val Ile Ser
130 135 140

ctg ccg ccc ctc atc tac aag ggc gac cag ggc ccc cag ccg cgc ggg	480
Leu Pro Pro Leu Ile Tyr Lys Gly Asp Gln Gly Pro Gln Pro Arg Gly	
145 150 155 160	
cgc ccc cag tgc aag ctc aac cag gag gcc tgg tac atc ctg gcc tcc	528
Arg Pro Gln Cys Lys Leu Asn Gln Glu Ala Trp Tyr Ile Leu Ala Ser	
165 170 175	
agc atc gga tct ttc ttt gct cct tgc ctc atc atg atc ctt gtc tac	576
Ser Ile Gly Ser Phe Phe Ala Pro Cys Leu Ile Met Ile Leu Val Tyr	
180 185 190	
ctg cgc atc tac ctg atc gcc aaa cgc agc aac cgc aga ggt ccc agg	624
Leu Arg Ile Tyr Leu Ile Ala Lys Arg Ser Asn Arg Arg Gly Pro Arg	
195 200 205	
gcc aag ggg ggg cct ggg cag ggt gag tcc aag cag ccc cga ccc gac	672
Ala Lys Gly Gly Pro Gly Gln Gly Glu Ser Lys Gln Pro Arg Pro Asp	
210 215 220	
cat ggt ggg gct ttg gcc tca gcc aaa ctg cca gcc ctg gcc tct gtg	720
His Gly Gly Ala Leu Ala Ser Ala Lys Leu Pro Ala Leu Ala Ser Val	
225 230 235 240	
gct tct gcc aga gag gtc aac gga cac tcg aag tcc act ggg gag aag	768
Ala Ser Ala Arg Glu Val Asn Gly His Ser Lys Ser Thr Gly Glu Lys	
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gag gag ggg gag acc cct gaa gat act ggg acc cgg gcc ttg cca ccc	816
Glu Glu Gly Glu Thr Pro Glu Asp Thr Gly Thr Arg Ala Leu Pro Pro	
260 265 270	
agt tgg gct gcc ctt ccc aac tca ggc cag ggc cag aag gag ggt gtt	864
Ser Trp Ala Ala Leu Pro Asn Ser Gly Gln Gly Gln Lys Glu Gly Val	
275 280 285	
tgt ggg gca tct cca gag gat gaa gct gaa gag gag gaa gag gag gag	912
Cys Gly Ala Ser Pro Glu Asp Glu Ala Glu Glu Glu Glu Glu Glu Glu	
290 295 300	
gag gag tgt gaa ccc cag gca gtg cca gtg tct ccg gcc tca gct tgc	960
Glu Glu Cys Glu Pro Gln Ala Val Pro Val Ser Pro Ala Ser Ala Cys	
305 310 315 320	
agc ccc ccg ctg cag cag cca cag ggc tcc cgg gtg ctg gcc acc cta	1008
Ser Pro Pro Leu Gln Gln Pro Gln Gly Ser Arg Val Leu Ala Thr Leu	
325 330 335	
cgt ggc cag gtg ctc ctg ggc agg ggc gtg ggt gct ata ggt ggg cag	1056
Arg Gly Gln Val Leu Leu Gly Arg Gly Val Gly Ala Ile Gly Gly Gln	
340 345 350	
tgg tgg cgt cga cgg gcg cag ctg acc cgg gag aag cgc ttc acc ttc	1104
Trp Trp Arg Arg Arg Ala Gln Leu Thr Arg Glu Lys Arg Phe Thr Phe	
355 360 365	
gtg ctg gct gtg gtc att ggc gtt ttt gtg ctc tgc tgg ttc ccc ttc	1152
Val Leu Ala Val Val Ile Gly Val Phe Val Leu Cys Trp Phe Pro Phe	
370 375 380	

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ttc ttc agc tac agc ctg ggc gcc atc tgc ccg aag cac tgc aag gtg 1200
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385 390 395 400

ccc cat ggc ctc ttc cag ttc ttc ttc tgg atc ggc tac tgc aac agc 1248
Pro His Gly Leu Phe Gln Phe Phe Phe Trp Ile Gly Tyr Cys Asn Ser
405 410 415

tca ctg aac cct gtt atc tac acc atc ttc aac cag gac ttc cgc cgt 1296
Ser Leu Asn Pro Val Ile Tyr Thr Ile Phe Asn Gln Asp Phe Arg Arg
420 425 430

gcc ttc cgg agg atc ctg tgc cgc ccg tgg acc cag acg gcc tgg tga 1344
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<212> PRT
<213> Homo sapiens

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Val Ile Leu Ala Val Leu Thr Ser Arg Ser Leu Arg Ala Pro Gln Asn
35 40 45

Leu Phe Leu Val Ser Leu Ala Ala Ala Asp Ile Leu Val Ala Thr Leu
50 55 60

Ile Ile Pro Phe Ser Leu Ala Asn Glu Leu Leu Gly Tyr Trp Tyr Phe
65 70 75 80

Arg Arg Thr Trp Cys Glu Val Tyr Leu Ala Leu Asp Val Leu Phe Cys
85 90 95

Thr Ser Ser Ile Val His Leu Cys Ala Ile Ser Leu Asp Arg Tyr Trp
100 105 110

Ala Val Ser Arg Ala Leu Glu Tyr Asn Ser Lys Arg Thr Pro Arg Arg
115 120 125

Ile Lys Cys Ile Ile Leu Thr Val Trp Leu Ile Ala Ala Val Ile Ser
130 135 140

Leu Pro Pro Leu Ile Tyr Lys Gly Asp Gln Gly Pro Gln Pro Arg Gly
145 150 155 160

Arg Pro Gln Cys Lys Leu Asn Gln Glu Ala Trp Tyr Ile Leu Ala Ser
165 170 175

Ser Ile Gly Ser Phe Phe Ala Pro Cys Leu Ile Met Ile Leu Val Tyr
180 185 190

Leu Arg Ile Tyr Leu Ile Ala Lys Arg Ser Asn Arg Arg Gly Pro Arg
195 200 205

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Ala Lys Gly Gly Pro Gly Gln Gly Glu Ser Lys Gln Pro Arg Pro Asp
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 His Gly Gly Ala Leu Ala Ser Ala Lys Leu Pro Ala Leu Ala Ser Val
 225 230 235 240
 Ala Ser Ala Arg Glu Val Asn Gly His Ser Lys Ser Thr Gly Glu Lys
 245 250 255
 Glu Glu Gly Glu Thr Pro Glu Asp Thr Gly Thr Arg Ala Leu Pro Pro
 260 265 270
 Ser Trp Ala Ala Leu Pro Asn Ser Gly Gln Gly Gln Lys Glu Gly Val
 275 280 285
 Cys Gly Ala Ser Pro Glu Asp Glu Ala Glu Glu Glu Glu Glu Glu
 290 295 300
 Glu Glu Cys Glu Pro Gln Ala Val Pro Val Ser Pro Ala Ser Ala Cys
 305 310 315 320
 Ser Pro Pro Leu Gln Gln Pro Gln Gly Ser Arg Val Leu Ala Thr Leu
 325 330 335
 Arg Gly Gln Val Leu Leu Gly Arg Gly Val Gly Ala Ile Gly Gly Gln
 340 345 350
 Trp Trp Arg Arg Arg Ala Gln Leu Thr Arg Glu Lys Arg Phe Thr Phe
 355 360 365
 Val Leu Ala Val Val Ile Gly Val Phe Val Leu Cys Trp Phe Pro Phe
 370 375 380
 Phe Phe Ser Tyr Ser Leu Gly Ala Ile Cys Pro Lys His Cys Lys Val
 385 390 395 400
 Pro His Gly Leu Phe Gln Phe Phe Phe Trp Ile Gly Tyr Cys Asn Ser
 405 410 415
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<210> 3

<211> 1353

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1350)

<223> Coding sequence for human alpha-2B-adrenoceptor protein

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 Met Asp His Gln Asp Pro Tyr Ser Val Gln Ala Thr Ala Ala Ile Ala
 1 5 10 15

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ctg ttc ctg gtg tcg ctg gcc gcc gcc gac atc ctg gtg gcc acg ctc Leu Phe Leu Val Ser Leu Ala Ala Ala Asp Ile Leu Val Ala Thr Leu 50 55 60	192
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cgc ccc cag tgc aag ctc aac cag gag gcc tgg tac atc ctg gcc tcc Arg Pro Gln Cys Lys Leu Asn Gln Glu Ala Trp Tyr Ile Leu Ala Ser 165 170 175	528
agc atc gga tct ttc ttt gct cct tgc ctc atc atg atc ctt gtc tac Ser Ile Gly Ser Phe Phe Ala Pro Cys Leu Ile Met Ile Leu Val Tyr 180 185 190	576
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gag gag ggg gag acc cct gaa gat act ggg acc cgg gcc ttg cca ccc	816
Glu Glu Gly Glu Thr Pro Glu Asp Thr Gly Thr Arg Ala Leu Pro Pro	
260 265 270	
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Ser Trp Ala Ala Leu Pro Asn Ser Gly Gln Gly Gln Lys Glu Gly Val	
275 280 285	
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Cys Gly Ala Ser Pro Glu Asp Glu Ala Glu Glu Glu Glu Glu Glu	
290 295 300	
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Glu Glu Glu Glu Glu Cys Glu Pro Gln Ala Val Pro Val Ser Pro Ala	
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Ser Ala Cys Ser Pro Pro Leu Gln Gln Pro Gln Gly Ser Arg Val Leu	
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Ala Thr Leu Arg Gly Gln Val Leu Leu Gly Arg Gly Val Gly Ala Ile	
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ggt ggg cag tgg tgg cgt cga cgg gcg cag ctg acc cgg gag aag cgc	1104
Gly Gly Gln Trp Trp Arg Arg Ala Gln Leu Thr Arg Glu Lys Arg	
355 360 365	
ttc acc ttc gtg ctg gct gtg gtc att ggc gtt ttt gtg ctc tgc tgg	1152
Phe Thr Phe Val Leu Ala Val Val Ile Gly Val Phe Val Leu Cys Trp	
370 375 380	
ttc ccc ttc ttc ttc agc tac agc ctg ggc gcc atc tgc ccg aag cac	1200
Phe Pro Phe Phe Phe Ser Tyr Ser Leu Gly Ala Ile Cys Pro Lys His	
385 390 395 400	
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Cys Lys Val Pro His Gly Leu Phe Gln Phe Phe Phe Trp Ile Gly Tyr	
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Cys Asn Ser Ser Leu Asn Pro Val Ile Tyr Thr Ile Phe Asn Gln Asp	
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ttc cgc cgt gcc ttc cgg agg atc ctg tgc cgc ccg tgg acc cag acg	1344
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Ala Trp	
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<210> 4

<211> 450

<212> PRT

<213> Homo sapiens

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Met Asp His Gln Asp Pro Tyr Ser Val Gln Ala Thr Ala Ala Ile Ala
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Ala Ala Ile Thr Phe Leu Ile Leu Phe Thr Ile Phe Gly Asn Ala Leu
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Val Ile Leu Ala Val Leu Thr Ser Arg Ser Leu Arg Ala Pro Gln Asn
35 40 45

Leu Phe Leu Val Ser Leu Ala Ala Ala Asp Ile Leu Val Ala Thr Leu
50 55 60

Ile Ile Pro Phe Ser Leu Ala Asn Glu Leu Leu Gly Tyr Trp Tyr Phe
65 70 75 80

Arg Arg Thr Trp Cys Glu Val Tyr Leu Ala Leu Asp Val Leu Phe Cys
85 90 95

Thr Ser Ser Ile Val His Leu Cys Ala Ile Ser Leu Asp Arg Tyr Trp
100 105 110

Ala Val Ser Arg Ala Leu Glu Tyr Asn Ser Lys Arg Thr Pro Arg Arg
115 120 125

Ile Lys Cys Ile Ile Leu Thr Val Trp Leu Ile Ala Ala Val Ile Ser
130 135 140

Leu Pro Pro Leu Ile Tyr Lys Gly Asp Gln Gly Pro Gln Pro Arg Gly
145 150 155 160

Arg Pro Gln Cys Lys Leu Asn Gln Glu Ala Trp Tyr Ile Leu Ala Ser
165 170 175

Ser Ile Gly Ser Phe Phe Ala Pro Cys Leu Ile Met Ile Leu Val Tyr
180 185 190

Leu Arg Ile Tyr Leu Ile Ala Lys Arg Ser Asn Arg Arg Gly Pro Arg
195 200 205

Ala Lys Gly Gly Pro Gly Gln Gly Glu Ser Lys Gln Pro Arg Pro Asp
210 215 220

His Gly Gly Ala Leu Ala Ser Ala Lys Leu Pro Ala Leu Ala Ser Val
225 230 235 240

Ala Ser Ala Arg Glu Val Asn Gly His Ser Lys Ser Thr Gly Glu Lys
245 250 255

Glu Glu Gly Glu Thr Pro Glu Asp Thr Gly Thr Arg Ala Leu Pro Pro
260 265 270

Ser Trp Ala Ala Leu Pro Asn Ser Gly Gln Gly Gln Lys Glu Gly Val
275 280 285

Cys Gly Ala Ser Pro Glu Asp Glu Ala Glu Glu Glu Glu Glu Glu
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Glu Glu Glu Glu Glu Cys Glu Pro Gln Ala Val Pro Val Ser Pro Ala
305 310 315 320

Ser Ala Cys Ser Pro Pro Leu Gln Gln Pro Gln Gly Ser Arg Val Leu
 325 330 335
 Ala Thr Leu Arg Gly Gln Val Leu Leu Gly Arg Gly Val Gly Ala Ile
 340 345 350
 Gly Gly Gln Trp Trp Arg Arg Arg Ala Gln Leu Thr Arg Glu Lys Arg
 355 360 365
 Phe Thr Phe Val Leu Ala Val Val Ile Gly Val Phe Val Leu Cys Trp
 370 375 380
 Phe Pro Phe Phe Phe Ser Tyr Ser Leu Gly Ala Ile Cys Pro Lys His
 385 390 395 400
 Cys Lys Val Pro His Gly Leu Phe Gln Phe Phe Phe Trp Ile Gly Tyr
 405 410 415
 Cys Asn Ser Ser Leu Asn Pro Val Ile Tyr Thr Ile Phe Asn Gln Asp
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 Ala Trp
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<210> 5
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: PCR primer pair

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<210> 6
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 <212> DNA
 <213> Artificial Sequence

<220>
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 <213> Artificial Sequence

<220>
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18

<210> 8
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<220>
<223> Description of Artificial Sequence: PCR primer pair

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<211> 21
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<223> Description of Artificial Sequence: PCR primer pair

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